

HUMAN xiap

SEQ ID: NO:4 a

STENSES

a K T C V P A D I N K E E F F V E E F N R

a L K T F A N F P S G S P V S A S T L A R

a A G F L Y T G E G D T V R C F S C H A A

a V D R W Q Y G D S A V G R H R K V S P N

a C R F I N G F Y L E N S A T Q S T N S C

FIG. 1 (PAGE 1 OF 7)

HUMAN xiap

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361  atccagaatggtcagtaacaaagtgaataactatctgtggaagcagagatcatttgcctta
a      I Q N G Q Y K V E N Y L G S R D H F A L
421  gacaggccatctgagacacatgcagactatcttttgagaactgggcagggtttagatatata
a      D R P S E T H A D Y L L R T G Q V V D I
481  tcagacacatataccgaggaaccctgccatgtattgtgaagaagctagattaaagtcc
a      S D T I Y P R N P A M Y C E E A R L K S
541  ttccagaactggccagactatgctcacctaaccaccaagagagtagcaagtgtggactc
a      F Q N W P D Y A H L T P R E L A S A G L
601  tactacacagggtattggtgaccaagtgcaagtgcttttgtgtgtggaaaactgaaaaat
a      Y Y T G I G D Q V Q C F C C G G K L K N
661  tgggaaccttgtgatcgtgcctggtcagaacacagcgacactttcctaattgcttctttt
a      W E P C D R A W S E H R R R H F P N C F F

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FIG. 1 (PAGE 2 OF 7)

HUMAN xiap

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gttttggccggaatcttaatatcgaagtgaatctgatgctgtgagttctgataggaat 721
a      V L G R N L N I R S E S D A V S S D R N -
      ttcccaaatcaacaaatcttccaagaatacccatccatggcagattatgaagcacggatc 781
a      F P N S T N L P R N P S M A D Y E A R I -
      ttactctttgggacatggatatatactcagttaacaaggagcagcttgcaagagctggattt 841
a      F T F G T W I Y S V N K E Q L A R A G F -
      tatgctttaggtgaaggtgataaaagtgtcttccactgtggaggaggcctaactgat 901
a      Y A L G E G D K V K C F H C G G G L T D -
      tggaagcccagtgaaagacccttggaacaacatgctaaatggatccagggtgcaaatat 961
a      W K P S E D P W E Q H A K W Y P G C K Y -
      ctgtagaacagaaggacaagaatatataaacaatatcatttaactcattcacttgag 1021
a      L L E Q K G Q E Y I N N I H L T H S L E -

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FIG. 1 (PAGE 3 OF 7)

HUMAN xiap

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1081 gagtgtctggttaagaactactgagaaaaacaccatcactaactagaagaattgatatacc 1140
      E C L V R T T E K T P S L T R R I D D T -
1141 atcttccaaaatcctatggtacaagaagctatacgaatgggttcagtttcaaggacatt 1200
      I F Q N P M V Q E A I R M G F S F K D I -
1201 aagaaaaataatggaggaaaaaattcagatatctgggagcaactataaatacacttgaggtt 1260
      K K I M E E K I Q I S G S N Y K S L E V -
1261 ctggttcagatctagtgaatgctcagaaaagacagtatgcaagatgagtcagagact 1320
      L V A D L V N A Q K D S M Q D E S S Q T -
1321 tcattacagaaagagattagtactgaagagcagctaaggcgctgcaagaggagaagctt 1380
      S L Q K E I S T E E Q L R R L Q E E K L -
1381 tgcaaaaatctgtatggatagaaaataattgctatcgttttgttccttgtggacatctagtc 1440

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FIG. 1 (PAGE 4 OF 7)

HUMAN xiap

1801 attcatagtatactgatttaatttctaagtgtaagtgaattaatcatctggatttttat + 1860

a

1861 tcttttcagataggcttaacaaatggagcttctgtatatataaatgtggagattagagtta + 1920

a

1921 atctcccaatcacataatttgttttgtgtgaaaaaggaaataaattgttccatgctggtg + 1980

a

1981 gaaagatagagattgttttttagaggttggttggtgtgttttaggattctgtccattttct + 2040

a

2041 tgtaagnnataaacacgnacntgtgcgaaatatntttgtaaagtgttggccattnttg + 2100

a

2101 aaagcgtatttaatgatagaatactatcgcagccaaacatgtactgacatggaaagatgtca + 2160

a

FIG. 1 (PAGE 6 OF 7)

HUMAN hiap-1

SEQ ID NO:5

1 TCCTTGAGATGATCAGTATAGGATTTAGGATCTCCATGTTGGAACCTCTAAATGCATAGA
60

C

61 AATGGAATAATGGAAATTTTTCATTTTGGCTTTTCAGCCTAGTATTAACCTGATAAAA
120

C

121 GCAAAGCCATGCACAAACTACCTCCCTAGAGAAAGGCTAGTCCCTTTCTTCCCCATTC
180

C

181 ATTCATTATGAACATAGTAGAAAACAGCATATTCTTATCAAAATTTGATGAAAAGCGCCA
240

SEQ ID NO:6 C

M N I V E N S I F L S N L M K S A N -

241 ACACGTTTGAACCTGAAATACGACTTGTCAATGTGAACCTGTACCGAATGTCTACGTATTCCA
300

C

T F E L K Y D L S C E L Y R M S T Y S T -

301 CTTTCCCTGCTGGGGTTCCTGTCTCAGAAAGGAGTCTTGCTCGTGTGTTCTATTACA
360

C

F P A G V P V S E R S L A R A G F Y Y T -

FIG. 2 (PAGE 1 OF 8)

HUMAN hiap-1

361	CTGGTGTGAATGACAAGGTCAAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAAA	420
	G V N D K V K C F C C G L M L D N W K R -	
421	GAGGAGACAGTCCCTACTGAAAAGCATAAAAAGTTGTATCCTAGCTGCAGATTTCGTTTCAGA	480
	G D S P T E K H K K L Y P S C R F V Q S -	
481	GTCATAATCCGGTTAACTTGGAAAGCTACCTCTCAGCCTACTTTTCTCTTCAGTAA	540
	L N S V N N L E A T S Q P T F P S S V T -	
541	CACATTCCACACACTCATCTCCGGGTACAGAAAACAGTGGATATTCCGGTGGCTCTT	600
	H S T H S L L P G T E N S G Y F R G S Y -	
601	ATTCAAACCTCTCCATCAAATCCCTGTAAACTCCAGAGCAAATCAAGAAATTTCTGCCCTTGA	660
	S N S P S N P V N S R A N Q E F S A L M -	
661	TGAGAAGTTCCTACCCCTGTCCAATGAATAACGAAAATGCCAGATTACTTACTTTTCAGA	720
	R S S Y P C P M N N E N A R L L T F Q T -	

FIG. 2 (PAGE 2 OF 8)

HUMAN hiap-1

721	C	CATGGCCATTGACTTTCTGTGCGCAACAGATCTGGCACGAGCAGGCTTTTACTACATAG	780
		W P L T F L S P T D L A R A G F Y Y I G -	
781		GACCTGGAGACAGAGTGGCTTGTGCTTGGTGGGAAATTGAGCAATTGGGAACCGA	840
		P G D R V A C F A C G G K L S N W E P K -	
841	C	AGGATAATGCTATGTCAGAACACCTGAGACATTTTCCCAAATGCCCATTTATAGAAAATC	900
		D N A M S E H L R H F P K C P F I E N Q -	
901		AGCTTCAAGACACTTCAAGATACACAGTTTCTAATCTGAGCATGCAGACACATGCAGCCCC	960
		L Q D T S R Y T V S N L S M Q T H A A R -	
961	C	GCTTTAAACATTCTTAACTGGCCCTCTAGTGTCTAGTTAATCCTGAGCAGCTTGCAA	1020
		F K T F F N W P S S V L V N P E Q L A S -	
1021	C	GTGCGGGTTTTTATTATGTGGGTAACAGTGATGATGTCAAAATGCTTTTGCTGTGATGGTG	1080
		A G F Y Y V G N S D D V K C F C C D G G -	

FIG. 2 (PAGE 3 OF 8)

HUMAN hiap-1

1081	GACTCAGGTGTGGGAATCTGGAGATGATCCATGGGTCAACATGCCAAGTGTTCCAA	1140
C	L R C W E S G D D P W V Q H A K W F P R -	
1141	GGTGTGAGTACTTGATAAGAAATTAAGGACAGGAGTTTCATCCGTCAAGTTCAAGCCAGTT	1200
C	C E Y L I R I K G Q E F I R Q V Q A S Y -	
1201	ACCCATCATCTACTTGAACAGCTGCTATCCACATCAGACAGCCAGGAGATGAAATGCAG	1260
C	P H L L E Q L L S T S D S P G D E N A E -	
1261	AGTCATCAATTATCCATTGGAACTGGAGAAGACCATTCAAGAAGATGCAATCATGATGA	1320
C	S S I I H L E P G E D H S E D A I M M N -	
1321	ATACTCCTGTGATTAAATGCTGCCGTGGAAATGGGCTTTAGTAGAAGCCCTGGTAAACAGA	1380
C	T P V I N A A V E M G F S R S L V K Q T -	
1381	CAGTTCAGAGAAAAATCCTAGCAACTGGAGAGAAATTATAGACTAGTCAATGATCTTGTGT	1440
C	V Q R K I L A T G E N Y R L V N D L V L -	

FIG. 2 (PAGE 4 OF 8)

HUMAN hiap-1

1441	TAGACTTACTCAATGCAGAAGATGAAATAAGGGAAGAGGAGAGAGAAAGCAACTGAGG	1500
C	D L L N A E D E I R E E E R A T E E -	
1501	AAAAAGAATCAATGATTATTATTATCCGGAAGAATAGAAATGGCACTTTTTCACACATT	1560
C	K E S N D L L L I R K N R M A L F Q H L -	
1561	TGACTTGTGTAAATCCCAATCCCTGGATAGTCTACTAACTGCCGGAATTATTATGAACAAG	1620
C	T C V I P I L D S L L T A G I I N E Q E -	
1621	AACATGATGTTATTAACAGAAGACACAGACGCTTTACAAGCAAGAGAACTGATTGATA	1680
C	H D V I K Q K T Q T S L Q A R E L I D T -	
1681	CGATTTAGTAAAGGAAATATTGCAGCCACTGTATTTCAGAAACTCTCTGCAAGAAAGCTG	1740
C	I L V K G N I A A T V F R N S L Q E A E -	
1741	AAGCTGTGTATATGAGCATTTATTGTGTCAACAGGACATATAATATATTCACACAGAAG	1800
C	A V L Y E H L F V Q Q D I K Y I P T E D -	

FIG. 2 (PAGE 5 OF 8)

HUMAN hiap-1

1801	ATGTTTCAGATCTACCAGTGAAGAACAATTGCGGAGACTACCAGAAGAAACAATGTA	1860
	V S D L P V E E Q L R R L P E E R T C K -	
1861	AAGTGTGTATGGACAAAGAAGTGTCCTAGTGTATTATTCCTTGTGGTCATCTAGTAGTAT	1920
	V C M D K E V S I V F I P C G H L V V C -	
1921	GCAAAGATTGTGCTCCTTCTTAAGAAAGTGTCCTATTTGTAGGAGTACAATCAAGGGTA	1980
	K D C A P S L R K C P I C R S T I K G T -	
1981	CAGTTCGTACATTTCTTCATGAAGAAGAACCAACATCGTCTAAACTTTAGAAATTAAT	2040
	V R T F L S *	
2041	TTATTAAATGTATTATAACTTTAACTTTTATCCTAATTGGTTTCCTTAAATTTTATT	2100
	TATTACAAC TCAAAAACATTGTTTGTGTAAACATATTTATATATGTATCTAAACCATA	2160

FIG. 2 (PAGE 6 OF 8)

SECRET

HUMAN hiap-1

2161 TGAACATATATTTTAGAACTAAGAGAATGATAGGCTTTTGTCTTATGAACGAAAA 2220

2221 GAGGTAGCACTACAAACACAAATATTCAATCCAAATTTCAGCATTTATTGAAATTGTAAGTG 2280

AAGTAAACTTAAGATATTGAGTTAACCTTTAAGAATTTAAATATTTGGCATTGTAC
2281 -----+-----+-----+-----+-----+-----+ 2340

2341 TAATACCGGAACATGAAGCCAGGTGTTGGTATGTACCTGTAGTCCCAGGCTGAGGCA 2400

2401 AGAGAAATTACTTGAGCCCCAGGAGTTGAATCCATCCTGGGCAGCATACTGAGACCCCTGCC 2460

2461 TTTAAACXACAGXACCAAAAXCCAACACCGGACACATTCTCTGTCTTTTGTAT 2520

FIG. 2 (PAGE 7 OF 8)

FIG. 2 (PAGE 7 OF 8)

HUMAN hiap-1

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2521  CAGTGTCCTATACATCGAAGGTGTCATATATGTTGAATCACATTTAGGACATGGTGT 2580
      -----+-----+-----+-----+-----+-----+
2581  TTTTATAAGAAATCTGTGAGXAAAAATTTAATAAGCAACCXAAATTACTCTTAAAAAA 2640
      -----+-----+-----+-----+-----+-----+
2641  AAAAAAAAAAAAAAACTCGAGGGGCCCCGTACCAAT 2676
      -----+-----+-----+-----+-----+

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FIG. 2 (PAGE 8 OF 8)

HUMAN hiap-2

SEQ ID NO:7		TTAGGTTACCTGAAAGAGTTACTACAACCCCAAGAGTTGTGTTCTAAGTAGTATCTTGG	1	60
	a			-
		TAAATTCAGAGAGATACTCATCCTACCTGAATATAAACTGAGATAAATCCAGTAAAGAAAG	61	120
	a			-
		TGTAGTAAATTCACATAAGAGTCTATCATTTGATTCTTTTGTGGTGGAAATCTTAGTT	121	180
	a			-
		CATGTGAAGAAATTCATGTGAATGTTTAGCTATCAAAACAGTACTGTCACCTACTCATG	181	240
	a			M -
		CACAAAACCTGCCCTCCCAAGACTTTTCCCAGGTCCTCGTATCAAAACATTAAGAGTATA	241	300
SEQ ID NO:8	a	H K T A S Q R L F P G P S Y Q N I K S I		-
		ATGGAAGATAGCAGCATCTTGTGCAGATTGGACAAACAGCAACAAACAAAATGAAGTAT	301	360
	a	M E D S T I L S D W T N S N K Q K M K Y		-

FIG. 3 (PAGE 1 OF 7)

HUMAN hiap-2

361	GACTTTCCCTGTGAACTCTACAGAAATGTCTACATATTCAACTTCCCGCGGGTGCCT	420
a	D F S C E L Y R M S T Y S T F P A G V P	-
421	GTCTCAGAAAGGAGTCTTGCTCGTGGTGTCTTTTATTATATACTGGTGTGAATGACAAAGGTC	480
a	V S E R S L A R A G F Y Y T G V N D K V	-
481	AAATGCTTCTGTGTGGCCTGATGCTGGATAACTGGAAACTAGGAGACAGTCCCTATTCAA	540
a	K C F C C G L M L D N W K L G D S P I Q	-
541	AAGCATAAACAGCTATATCCTAGCTGTAGCTTTATTCAGAAATCTGGTTTCAGCTAGTCTG	600
a	K H K Q L Y P S C S F I Q N L V S A S L	-
601	GGATCCACCTCTAAGAAATACGCTCCCAATGAGAAACAGTTTGGCACATTCTATCTCCC	660
a	G S T S K N T S P M R N S F A H S L S P	-
661	ACCTTGGAACATAGTAGCTTGTTTCAGTGGTCTTACTCCAGCCTTCTCTCAAACCCCTCTT	720
a	T L E H S S L F S G S Y S S L P P N P L	-

FIG. 3 (PAGE 2 OF 7)

HUMAN hiap-2

	AATTCTAGAGCAGTTGAAGACATCTCTTCATCGAGGACTAACCCCTACAGTTATGCAATG	721	
a	N S R A V E D I S S R T N P Y S Y A M	780	
	AGTACTGAAGAAGCCAGATTCTTACCTACCATATGTGGCCATTAACTTTTGTCCACCA	840	
a	S T E E A R F L T Y H M W P L T F L S P	900	
	TCAGAATTGGCAAGAGCTGGTTTTATATATAGGACCTGGAGATAGGCTAGCCTGCTTT	960	
a	S E L A R A G F Y Y I G P G D R V A C F	1020	
	GCCTGTGTGGGAAGCTCAGTAACTGGGAACCAAGGATGCTATGTCAGAACACCGG	1080	
a	A C G G K L S N W E P K D D A M S E H R	1140	
	AGGCATTTCCCAACTGTCCATTTTGGAAAATTCTCTAGAAACTCTGAGGTTTAGCATT	1200	
a	R H F P N C P F L E N S L E T L R F S I	1260	
	TCAAATCTGAGCATGCAGACACATGCAGCTCGAATGAGAACAATTATGTACTGGCCATCT	1320	
a	S N L S M Q T H A A R M R T F M Y W P S	1380	

FIG. 3 (PAGE 3 OF 7)

HUMAN hiap-2

1081	AGTGTCCAGTTCAGCCTGAGCAGCTTGCAAGTGCTGGTTTATATATGTGGTCGCAAT	1140
a	S V P V Q P E Q L A S A G F Y Y V G R N	-
1141	GATGATGCAAAATGCTTTGGTTGTGATGGTGGCTTGAGGTGTGGGAATCTGGAGATGAT	1200
a	D D V K C F G C D G G L R C W E S G D D	-
1201	CCATGGGTAGAACATGCCAAGTGGTTTCCCAAGGTGTGAGTTCTTGATACGAATGAAAGGC	1260
a	P W V E H A K W F P R C E F L I R M K G	-
1261	CAAGAGTTTGTGATGAGATTCAAGGTAGATATCCTCATCTTCTTGAACAGCTGTTGTCA	1320
a	Q E F V D E I Q G R Y P H L L E Q L L S	-
1321	ACTTCAGATACCACTGGAGAGAAATGCTGACCCACCAATTATTCATTTTGGACCTGGA	1380
a	T S D T T G E E N A D P P I I H F G P G	-
1381	GAAAGTTCTCAGAAAGATGCTGTCATGATGAATACACCTGTGGTTAAATCTGCCCTTGAA	1440
a	E S S S E D A V M M N T P V V K S A L E	-

FIG. 3 (PAGE 4 OF 7)

HUMAN hiap-2

1441	ATGGGCTTAA	TAGAGACCTGGTGA	AAACACAGTTCTA	AGTAAAAATCCTG	ACAACTGGA	1500
a	M G F N R D L V K Q T V L S K I L T T G	-				
1501	GAGAACTATA	AAACAGTTAATG	ATATTGTGTCAG	CACCTTCTTAAT	GCTGAAGATGA	1560
a	E N Y K T V N D I V S A L L N A E D E K	-				
1561	AGAGAAAGAG	AAGGAAAAACA	AGCTGAAGAAAT	GGCATCAGATG	ATTGTTCATTA	1620
a	R E E E K E K Q A E E M A S D D L S L I	-				
1621	CGGAAGAACAG	AATGGCTCTCTT	TCACAAATGACA	TGTGTGCTTCCT	TATCCTGGATA	1680
a	R K N R M A L F Q Q L T C V L P I L D N	-				
1681	CTTTTAAAGG	CCAATGTAATT	ATAAACAGGAAC	ATGATATTATTA	ACAAAAACACAG	1740
a	L L K A N V I N K Q E H D I I K Q K T Q	-				
1741	ATACCTTTACA	AGCAGAGAACTG	ATTGATACCAT	TTGGTTAAAGG	AAATGCTGCGGCC	1800
a	I P L Q A R E L I D T I W V K G N A A A	-				

FIG. 3 (PAGE 5 OF 7)

HUMAN hiap-2

1801	AACATCTTCAAAACTGTCTAAAAGAAATTGACTCTACATTGTATAAGAACTTATTGTG	1860
a	N I F K N C L K E I D S T L Y K N L F V	-
1861	GATAAGAAATATGAAGTATATTCCACAGAGAAGATGTTTCAGGCTGTCTCACTGGAAGAACAA	1920
a	D K N M K Y I P T E D V S G L S L E E Q	-
1921	TTGAGGAGGTTGCAAGAAGAACGAACTTGTAAGTGATGACAAAGAAGTTCTCTGT	1980
a	L R R L Q E E R T C K V C M D K E V S V	-
1981	GTATTATTCCTTGTGGTCATCTGGTAGTATGCCAGGAATGTGCCCCCTTCTCTAAGAAA	2040
a	V F I P C G H L V V C Q E C A P S L R K	-
2041	TGCCCTATTTCAGGGGTATAATCAAGGGTACTGTTCGTACATTCTCTCTTAAAGAAA	2100
a	C P I C R G I I K G T V R T F L S *	-
2101	ATAGTCTATATTTAACCTGCATAAAAAGGCTCTTAAATAATTTGTTGAACACTTGAAGCC	2160
a		-

FIG. 3 (PAGE 6 OF 7)

HUMAN hiap-2

2161	ATCTAAAGTAAAAGGAATTATGAGTTTTTCAATTAGTAACATTCAATGTTCTAGTCTGC	2220
a	-	-
2221	TTTGGTACTAATAATCTTGTCTGAAAAGATGGTATCATATATTAACTCTTAATCTGTT	2280
a	-	-
2281	TATTACAAGGGAAGATTATGTTTGGTGAACATATATAGTATGTGTACCTAAGGG	2340
a	-	-
2341	AGTAGCGTCXCTGCTTGTATGCATCATTTTCAGGAGTTACTGGATTTGTTGTTCTTTCAG	2400
a	-	-
2401	AAAGCCTTTGAAXACTAAATTATAGTGTAGAAAAGAACTGGAAACCAGGAACCTCTGGAGTT	2460
a	-	-
2461	CATCAGAGTTATGGTGCCGAATTGTCTTTGGTGCTTTTCACTTGTTGTTTAAATAAGGA	2520
a	-	-
2521	TTTTTCTCTTATTTCTCCCCCTAGTTTGTGAGAAACATCTCAATAAAGTCCTTAAAAAG	2580
a	-	-

FIG. 3 (PAGE 7 OF 7)

MOUSE xiap

SEQ ID NO:9

GACTCTGCTGGCGGGCGGCCCTCCTCCGGACCTCCCCCTCGGAACCGTCGCCC
1 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + - - - - - +

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CGGGCGCTTAGT TAGGACTGGAGTGCTTGGCGCGGAAGAAGGTGGACAAGTCCTATTTTCCA
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+
61 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 120

॥

GAGAAGATGACTTTTAACAGTTTGAAGGAAGTCTTGTACTTGCAGACACCAAT
 121
 180

SEQ ID NO:10 a

M T F N S F E G T R T F V L A D T N

AAGGATGAAGAAATTGTAGAGAGGTTTAATAGATTAAAAACATTGCTAACTTCCCAAGT
181

10

K D E E F V E E F N R L K T F A N F P S

AGTAGTCCCTGTTTCAGCATCAACATTGGCGCGAGCTGGGTTCTTTATACCGTGAAGGA
241 -----+-----+-----+-----+-----+-----+-----+ 300

३

S S P V S A S T L A R A G F L Y T G E G

GACACCGTCAATGTTTCAGTTGTCAATGCGCAATAGATAGATGGCAGTATGGAGACTCA
301

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D T V Q C C F S C H A A I D R W Q Y G D S S

FIG. 4 (PAGE 1 OF 6)

MOUSE xiap

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361  GCTGTTGGAAGACACAGGAGAAATATCCCCAAATTCAGATTTATCAATGGTTTATTTT 420
      A V G R H R R I S P N C R F I N G F Y F -
421  GAAATGGTGCTGCACAGTCTACAAATCCTGGTATCCAAATGGCCAGTACAAATCTGAA 480
      E N G A A Q S T N P G I Q N G Q Y K S E -
481  AACTGTGTGGGAAATAGAAATCCTTTTGCCCTTGACAGGCCACCTGAGACTCATGCTGAT 540
      N C V G N R N P F A P D R P P E T H A D -
541  TATCTCTTGAGAACTGGACAGGTTGTAGATATTTTCAGACACCATATACCCGAGGAACCT 600
      Y L L R T G Q V V D I S D T I Y P R N P -
601  GCCATGTGTAGTGAAGAAGCCAGATTGAAGTCATTCAGAACTGCCCGACTATGCTCAT 660
      A M C S E E A R L K S F Q N W P D Y A H -
661  TTAACCCCCAGAGAGTTAGCTAGTGGCTGCTTACTACACAGGGGCTGATCAAGTG 720
      L T P R E L A S A G L Y Y T G A D D Q V -

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FIG. 4 (PAGE 2 OF 6)

MOUSE xiap

721	CAATGCTTTTGTGGGGAAACTGAAAAATTGGAAACCCTGTGATCGTGCCTGGTCA	780
a	Q C F C C G G K L K N W E P C D R A W S	-
781	GAACACAGGAGACACTTCCCAATGCTTTTGTGTTTGGGCCGGAACGTTAATGTTCCGA	840
a	E H R R H F P N C F F V L G R N V N V R	-
841	AGTGAATCTGGTGTGAGTTCTGATAGGAATTCCCCAAATTCAACAACTCTCCAAGAAAT	900
a	S E S G V S S D R N F P N S T N S P R N	-
901	CCAGCCATGGCAGAAATATGAAGCACGGATCGTTACTTTTGGAACATGGATATACTCAGTT	960
a	P A M A E Y E A R I V T F G T W I Y S V	-
961	AACAAGGAGCAGCTTGCAAGAGCTGGATTTTATGCTTTAGGTGAAGGCCGATAAAGTGAAG	1020
a	N K E Q L A R A G F Y A L G E G D K V K	-
1021	TGCTTCCACTGTGGAGGGCTCACGGATTGGAAGCCCAAGTGAAGACCCCTGGACCAG	1080
a	C F H C G G G L T D W K P S E D P W D Q	-

FIG. 4 (PAGE 3 OF 6)

MOUSE xiap

1081	CATGCTAAGTGTACCCAGGTGCAAAATACCTATTGGATGAGAAGGGCAAGATATATA	1140
a	H A K C Y P G C K Y L L D E K G Q E Y I	-
1141	AATAATATTCAATTAACCCATCCACTTGAGGAATCTTTGGGAAGAACTGCTGAAAAACA	1200
a	N N I H L T H P L E E S L G R T A E K T	-
1201	CCACCGCTAACTAAAAATCGATGATACCATCTTCCAGAAATCCTATGGTGCAAGAAGCT	1260
a	P P L T K K I D D T I F Q N P M V Q E A	-
1261	ATACGAATGGGATTAGCTTCAAGGACCTTAAGAAAAACAATGGAAGAAAAATCCAACA	1320
a	I R M G F S F K D L K K T M E E K I Q T	-
1321	TCCGGGAGCAGCTATCTATCACTTGAGGTCCTGATTCAGATCTTGTGAGTGTCTCAGAAA	1380
a	S G S S Y L S L E V L I A D L V S A Q K	-
1381	GATAATACGAGGATGAGTCAAGTCAAACTTCAATTCAGAAAGACATTAGTACTGAAGAG	1440
a	D N T E D E S S Q T S L Q K D I S T E E	-

FIG. 4 (PAGE 4 OF 6)

MOUSE xiap

1441	CAGCTAAGGCGCTACAAGAGGAGAAGCTTCCAAATCTGTATGATAGAAATATTGCT	1500
a	Q L R R L Q E E K L S K I C M D R N I A	-
1501	ATCGTTTTTTTCTGTGGACATCTGGCCACTTGTAAACAGTGTGCAGAGCAGTTGAC	1560
a	I V F F P C G H L A T C K Q C A E A V D	-
1561	AAATGTCCCATGTGCTACACCGTCATTACGTTCAACCAAAATTTTATGTCTTAGTGG	1620
a	K C P M C Y T V I T F N Q K I F M S *	-
1621	GGCACCACATGTTATGTTCTTCTTGCTCTAATTGAATGTGTAATGGAGCGAACTTTAAG	1680
a		-
1681	TAATCCTGCATTTGCAATTCATTAGCATCCCTGCTGTTTCCAAATGGAGACCAATGCTAAC	1740
a		-
1741	AGCACTGTTTCCGCTAAACATTCAATTTCTGGATCTTTTCGAGTTATCAGCTGTATCATT	1800
a		-

FIG. 4 (PAGE 5 OF 6)

MOUSE xiap

1801	TAGCCAGTGTTTACTCGATTGAAACCTTAGACAGAGAAGCATTTTATAGCTTTTCACAT	1860
a	-	-
1861	GTATATTGGTAGTACACTGACTTGATTCTATATGTAAGTGAATTCATCACCCTGCATGTT	1920
a	-	-
1921	TCATGCCCTTTTGCAATAAGCTTAACAAATGGAGTGTTCTGTATAAGCATGGAGATGTGATG	1980
a	-	-
1981	GAATCTGCCCCAATGACTTTAATTGGCTTATTGTAAACACGGAAAGAACTGCCCCCACGCTG	2040
a	-	-
2041	CTGGGAGGATAAAGATTGTTTAGATGCTCACTTCTGTGTTTAGGATTCTGCCCATTTA	2100

FIG. 4 (PAGE 6 OF 6)

M-hiap-1

FIG. 5 (PAGE 1 OF 6)

M-hiap-1

```

CACAGAAAGTTGTACCCAGCTGCAACTTTGTACAGACTTTGAATCCAGCCAACAGCTG
421 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 480
H R K L Y P S C N F V Q T L N P A N S L -

GAAGCTAGTCCTCGGCCTTCTCTTCCACGGCGATGAGCACCATGCCCTTGAGCTTT
481 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 540
E A S P R P S L P S T A M S T M P L S F -

GCAAGTTCGAGAACTGGCTATTTCAGTGGCTCTTACTCGAGCTTTCCTCCAGACCT
541 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 600
A S S E N T G Y F S G S Y S S F P S D P -

GTGAACTTCGAGCAAAATCAAGATTGTCCTGCTTTGAGCACAAAGTCCCTACCATTGCA
601 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 660
V N F R A N Q D C P A L S T S P Y H F A -

ATGAACACAGAGAAGGCCAGATTACTCACCTATGAAACATGGCCATTGTCTTTCTGTCA
661 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 720
M N T E K A R L L T Y E T W P L S F L S -

CCAGCAAAGCTGGCCAAAGCAGGCTTCTACTACATAGACCTGGAGATAGAGTGCCCTGC
721 - - - - - + - - - - - + - - - - - + - - - - - + - - - - - + 780
P A K L A K A G F Y Y I G P G D R V A C -

```

FIG. 5 (PAGE 2 OF 6)

M-hiap-1

```

781 TTTGCGTGGGAACTGAGCAACTGGGAACGTAAGGATGATGCTATGTCAGAGCAC
-----+-----+-----+-----+-----+-----+-----+
F A C D G K L S N W E R K D D A M S E H - 840

841 CAGAGGCATTTCCCCAGCTGTCGTTCTTAAAAGACTTGGTCAGTCTGCTTCGAGATAC
-----+-----+-----+-----+-----+-----+-----+
Q R H F P S C P F L K D L G Q S A S R Y - 900

901 ACTGCTCTTAACCTGAGCATGCAGACACAGCCCGTATTAGAACATTCTCTAACTGG
-----+-----+-----+-----+-----+-----+-----+
T V S N L S M Q T H A A R I R T F S N W - 960

961 CCTTCTAGTGCAGTTCATTCAGGAAGTTCAGTCCGGGCTTTATTATACAGGA
-----+-----+-----+-----+-----+-----+-----+
P S S A L V H S Q E L A S A G F Y Y T G - 1020

1021 CACAGTGATGTCAAGTGTATTATGCTGTGATGGTGGGCTGAGTGTGGGAATCTGGA
-----+-----+-----+-----+-----+-----+-----+
H S D D V K C L C C D G G L R C W E S G - 1080

1081 GATGACCCCTGGTGGAACATGCCAAGTGGTTCCAAGGTGTGAGTACTGCTCAGAATC
-----+-----+-----+-----+-----+-----+-----+
D D P W V E H A K W F P R C E Y L L R I - 1140

1141 AAAGGCCAAGAATTGTGAGCCCAAGTTCAGCTGGCTATCCTCATCTACTTGAGCAGCTA
-----+-----+-----+-----+-----+-----+-----+
K G Q E F V S Q V Q A G Y P H L L E Q L - 1200

```

FIG. 5 (PAGE 3 OF 6)

M-hiap-1

1201	TTATCTACGTCACTCCCAGAAGATGAGAATGCAGACCGCAGCAATCGTGCAATTTGGC	1260
	L S T S D S P E D E N A D A A I V H F G	
1261	CCTGGAGAAAGTTCGGAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTTG	1320
	P G E S S E D V V M M S T P V V K A A L	
1321	GAAATGGGCTTCAGTAGGAGCCTGGTGAGACAGACGGTTCAGTGGCAGATCCTGGCCACT	1380
	E M G F S R S L V R Q T V Q W Q I L A T	
1381	GGTGAGAACTACAGGACCGTCAGTGACCTCGTTATAGGCTTACTCGATGCAGAAGACGAG	1440
	G E N Y R T V S D L V I G L L D A E D E	
1441	ATGAGAGAGGAGCAGATGGAGCAGCGCGCCGAGGAGGAGTCAGATGATCTAGCACTA	1500
	M R E E Q M E Q A A E E E E S D D L A L	
1501	ATCCGGAAGAACAAATGGTGCTTTTCCAACATTTGACGTGTGTGACACCAATGCTGTAT	1560
	I R K N K M V L F Q H L T C V T P M L Y	

FIG. 5 (PAGE 4 OF 6)

M-hiap-1

1561	TGCCTCCTAAGTGCAAGGCCATCACTGAACAGGAGTGCAATGCTGTGAAACAGAAACCA	1620
	C L L S A R A I T E Q E C N A V K Q K P	-
1621	CACACCTTACAAGCAAGCACACTGATTGATACTGTGTAGCAAAAGGAAACACTGCAGCA	1680
	H T L Q A S T L I D T V L A K G N T A A	-
1681	ACCTCATTCAGAAACTCCCTTCGGGAAATTGACCCCTCGTTATACAGAGATATTTGTG	1740
	T S F R N S L R E I D P A L Y R D I F V	-
1741	CAACAGGACATTAGGAGTCTTCCACAGATGACATTGCAGCTCTACCAATGGAAGAACAG	1800
	Q Q D I R S L P T D D I A A L P M E E Q	-
1801	TTGCGGCCCTCCCGAGGACAGAAATGTGTAAAGTGTGTATGGACCGAGAGGTATCCATC	1860
	L R P L P E D R M C K V C M D R E V S I	-
1861	GTGTTCAATCCCTGTGGCCATCTGGTCGTGTGCAAAAGACTGCGCTCCCTCTCTGAGGAAG	1920
	V F I P C G H L V V C K D C A P S L R K	-

FIG. 5 (PAGE 5 OF 6)

M-hiap-1

1921	TGTCCCATCTGTAGAGGACCATCAAGGCACAGTGGCCACATTTCTCTCTGAACAAGA	1980
	C P I C R G T I K G T V R T F L S *	-
1981	CTAATGGTCCATGGCTGCAACTTCAGCCAGGAGGAAGTTCACCTGTCACTCCCAGTTCCAT	2040
2041	TCGGAACTTGAGGCCAGCCTGGATAGCACGAGACACCCGCAACACACAAATATAAACAT	2100
2101	GAAAAACTTTTGTCTGAAGTCAAGAATGAATGAAATTAATAATAATTTAATTGGT	2160
2161	TTCCCTTAAAAGTGCTATTTGTTCCCAACTCAGAAAATTGTTTCTGTAAACATATTACA	2220
2221	TACTACCTGCATCTAAAGTATTTCATATATATTCATATATTCAGATGTCATGAGAGGGTTT	2280
2281	TGTTCTTGTTCCCTGAAAAGCTGGTTTATCATCTGTATCAGCATATATACTGCGCAACGGGCAG	2340
2341	GGCTAGAAATCCATGAACCAAGCTGCAAAGATCTCACGCTAAATAAGCGGAAAGATTGG	2400
2401	AGAAACGAAAGGAAATTCTTTCCCTGTCCAATGTATACTCTTCAGACTAATGACCCCTTCC	2460
2461	TATCAAGCCCTTCTA	
	-----+----- 2474	

FIG. 5 (PAGE 6 OF 6)

M-hiap-2

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421  GACTCTGCTTTCAGCCAGTCTGCAGTCTCCATCTAAGAATAATGTCTCTGTGAAAAGTAG 480
      T L L S A S L Q S P S K N M S P V K S R -
481  ATTTGCACATTGTCACCTCTGGAACGAGGTGGCATTCACTCCAACCTGTGCTCTAGCCC 540
      F A H S S P L E R G G I H S N L C S S P -
541  TCTTAATTCTAGAGCAGTGGAAAGACTTCTCATCAAGGATGGATCCCTGCAGCTATGCCAT 600
      L N S R A V E D F S S R M D P C S Y A M -
601  GAGTACAGAAGAGGCCAGATTCTTACTTACAGTATGTGGCCTTAAAGTTTCTGTCACC 660
      S T E E A R F L T Y S M W P L S F L S P -
661  AGCAGAGCTGGCCAGAGCTGGCTTCTATTACATAGGCCCTGGAGACAGGGTGGCCTGTTT 720
      A E L A R A G F Y Y I G P G D R V A C F -
721  TGCCTGTGTGGAAACTGAGCAACTGGGAACCAAGGATTATGCTATGTGAGACACCG 780
      A C G G K L S N W E P K D Y A M S E H R -

```

FIG. 6 (PAGE 2 OF 6)

M-hiap-2

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1141 CACTTCAGACACCCAGGAGAAATGCTGACCCCTACAGACAGTGGTGCATTTGG + 1200
      T S D T P G E E N A D P T E T V V H F G -
1201 CCCTGGAGAAAGTTTCGAAAGATGTCGTCATGATGAGCACGCCCTGTGGTTAAAGCAGCCTT + 1260
      P G E S S K D V V M M S T P V V K A A L -
1261 GGAATGGGCTTCAGTAGAGCCTGGTGAGACAGACGTTTCAGCGGCAGATCCTGGCCAC + 1320
      E M G F S R S L V R Q T V Q R Q I L A T -
1321 TGGTGAGAACTACAGACCGTCAATGATATTGTCTCAGTACTTTTGAATGCTGAAGATGA + 1380
      G E N Y R T V N D I V S V L L N A E D E -
1381 GAGAAAGAGAGGAGAGGAAAGACAGACTGAAGAGATGCCATCAGGTGACTTATCACT + 1440
      R R E E E K E R Q T E E M A S G D L S L -
1441 GATTGGAAGAAATAGATGCCCTCTTTCAACAGTTGACACATGTCCCTTCTATCCTGGA + 1500
      I R K N R M A L F Q Q Q L T H V L P I L D -

```

FIG. 6 (PAGE 4 OF 6)

M-hiap-2

1501	TAATCTTCTTGAGGCCAGTGTAATTACAAAACAGGAACATGATATTATTAGACAGAAAAC	1560
	N L L E A S V I T K Q E H D I I R Q K T	
1561	ACAGATACCCCTTACAAGCAAGAGAGCCTTATTGACACCGTTTTAGTCAAGGGAATGCTGC	1620
	Q I P L Q A R E L I D T V L V K G N A A	
1621	AGCCAACATCTTCAAAAACCTCTCTGAAGGAATTGACTCCACGTTATATGAAAACCTTATT	1680
	A N I F K N S L K G I D S T L Y E N L F	
1681	TGTGAAAAGAATATGAAGTATATTCCAACAGAAAGACGTTTCAGGCTTGTCATTGGAAGA	1740
	V E K N M K Y I P T E D V S G L S L E E	
1741	GCAGTTGCGGAGATTACAAGAAGAACGAACTTGCAAAAGTGTGTATGGACAGAGAGGTTTC	1800
	Q L R R L Q E E R T C K V C M D R E V S	
1801	TATTGTGTTTCATTCGGTGGTCATCTAGTAGTCTGCCAGGAATGTGCCCTTCTCTAAG	1860
	I V F I P C G H L V V C Q E C A P S L R	

FIG. 6 (PAGE 5 OF 6)

M-hiap-2

1861	GAAGTCCCCATCTGCAGGGGACAAATCAAGGGACTGTGCCACATTTCTCTCATGAGT	1920
	K C P I C R G T I K G T V R T F L S *	
1921	GAAGAATGGTCTGAAAGTATTGTTGGACATCAGAAGCTGTCAGAACAAAGAAATGAACCTAC	1980
1981	TGATTTACAGCTCTTCAGCAGGACATTTACTCTCTTTCAAGATTAGTAATCTTGCTTTTAT	2040
2041	GAAGGTAGCATTTGTATATTAAAGCTTAGTCTGTTGCAAGGGAAGTCTATGCTGTTGAG	2100
2101	CTACAGGACTGTGTCTGTTCCAGAGCAGGAGTTGGGATGCTTGCTGTATGTCTTCAGGA	2160
2161	CTTCTTGGGATTGGGAATTGGGAAAGCTTTGGAATCCAGTGATGTGGAGCTCAGAAA	2220
2221	TCCTGGAACCAAGTACTCTGTACTCAGTAGATAGGGTACCCTGTACTTCTTGGTGCTTT	2280
2281	TCCAGTCTGGGAAATAAGGAGGAAATCTGCTGCTGGTAAAAAATTGCTGGATGTGAGAAAT	2340
2341	AGATGAAAGTGTTCGGGTGGGGCGTGTCATCAGTGTAGTGTGTGCAGGGAATGTATGCAG	2400
2401	GCCAAACACTGTGTAG	
	-----+----- 2416	

FIG. 6 (PAGE 6 OF 6)

Alignment of BIR (Baculoviral IAP Repeats) Domains

Bacul virus

Cp_iap

Op_iap

Human

xiap

hiap1, hiap2

Mouse

m-xiap

Insect

diap

Cydia pomonella

Orgyia pseudotsugata

IAP on X chromosome

two different human IAP genes

mouse homologue of human xiap gene

Drosophila IAP gene, not clearly a homologue of xiap or hiap

FIG. 7

note on consensus: The consensus line represents amino acids or very similar amino acids which are present in 14 of the 19 BIR sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:11	Op_iap-1	1	kaarLgTttn	WPVqf.l	leps	rMAasGFYI	GrGDeVrCaf	CkveitnWtr	gDdpelDhtr	waPqCpFV	68
SEQ ID NO:14	Cp_iap-1		eevRLnTFek	WPVsf.l	ispe	tMAknGFYI	GrGDeVrCaf	CkveimrWke	gEdpaadHtk	waPqCpFV	
SEQ ID NO:15	diap-2		eanRLvTFkd	WPnbn.l	lPq	alABAGFYI	nrlDhVkcVw	CngvIakWek	nDnafeeHkr	ffPqCpRV	
SEQ ID NO:16	m-xiap-1		efnRLkTFan	FPssspvsas		tlARAGFLYt	GegDtVqCfs	ChaaIdrWqy	gDSavgrHrk	IsPnCrFI	
SEQ ID NO:17	xiap-1		efnRLkTFan	FPssspvsas		tlARAGFLYt	GegDtVrCfs	ChaaIdrWqy	gDSavgrHrk	vsPnCrFI	
SEQ ID NO:18	hiap1-1		elyRMsrYat	FPagvpsas		slARAGFYt	GvndkVkcFc	CgImIdnWkl	gDsptekHtk	lyPaCrFV	
SEQ ID NO:19	hiap2-1		elyRMsrYat	FPagvpsas		slARAGFYt	GvndkVkcFc	CgImIdnWkl	gDsptekHtk	lyPaCrFV	
SEQ ID NO:20	m-xiap-2		eearLksFqn	WPdyahltpr		elAaAGLYt	GadDqVqCfc	CggklnWep	cDrawseHrk	hfpnCrFV	
SEQ ID NO:21	xiap-2		eearLksFqn	WPdyahltpr		elAaAGLYt	GadDqVqCfc	CggklnWep	cDrawseHrk	hfpnCrFV	
SEQ ID NO:22	hiap1-2		eearLkTFtm	WP.lflslps		qlAaAGLYt	GpgDrVaCfa	CggklnWep	kDnamsEhlr	hfpnCrF1	
SEQ ID NO:23	hiap2-2		eearLkTFtm	WP.lflslps		qlAaAGLYt	GpgDrVaCfa	CggklnWep	kDnamsEhlr	hfpnCrF1	
SEQ ID NO:24	m-xiap-3		yeaRlVtFgt	Wlysv..nke		qlAaAGFYal	GegDkVkcFh	CgggltdWkp	sEdpweqHak	cyPgCkY1	
SEQ ID NO:25	xiap-3		yeaRlVtFgt	Wlysv..nke		qlAaAGFYal	GegDkVkcFh	CgggltdWkp	sEdpweqHak	wyPgCkY1	
SEQ ID NO:26	hiap1-3		haaRlVtFfn	WPssvlvnp		qlAaAGFYv	GnsDdVkcFc	CdggllrcWes	gDdpwvqHak	wfPrCay1	
SEQ ID NO:27	hiap2-3		haaRlVtFfn	WPssvlvnp		qlAaAGFYv	GnsDdVkcFc	CdggllrcWes	gDdpwvqHak	wfPrCay1	
SEQ ID NO:28	Op_iap-2		eearLkTFae	WPrglkqrpe		qlAaAGFYt	GqgDktrCfc	Cdggllkdwep	dnapwqHak	wydrCay1	
SEQ ID NO:29	Cp_iap-2		eearLkTFae	WPrglkqrpe		qlAaAGFYt	GqgDktrCfc	Cdggllkdwep	dnapwqHak	wydrCay1	
SEQ ID NO:30	diap-3		vdaRLrTFtd	WPisnlqpas		qlAaAGLYt	GygDntkCfy	Cdggllkdwep	eDvpweqHrk	widrCay1	
SEQ ID NO:31	diap-1		eevRLaTFge	WPInapvsas		qlAaAGLYt	GygDntkCfy	Cdggllkdwep	eDvpweqHrk	widrCay1	
SEQ ID NO:2	Consensus		---RL-TY--	WP-----		-LA-AGFYI-	G--D-V-CF-	C-----W--	-D-----H--	--P-C-FV	

	301	BIR 3				350
cp-lap	qrpeEQMAdAG	FFYtGyGDnt	KCFyCdGGLk	dWepeDvPWc	QHvrWFdrCa	
diap	qpasaLAqAG	LYYqkIGDcV	rCFhCnIGLr	swqkeDEPWf	eHAKWSPKQc	
m-xiap	VnxEQLArAG	FYalGeGDkV	KCFhCgGGLc	dWkpsEDPWd	QHAKcYPgCk	
xiap	VnxEQLArAG	FYalGeGDkV	KCFhCgGGLc	dWkpsEDPWc	QHAKWYPgCk	
hiap1	VnxEQLArAG	FYYvGnsDcV	KCFcCdGGLr	cWesgDDPWv	QHAKWFPgCe	
hiap2	VnxEQLArAG	FYYvGnsDcV	KCFcCdGGLr	cWesgDDPWv	eHAKWFPgCe	
consensus	V---EQLA--AG	FYY--G--GD--V	KCF--C--GGL--	--W---DDPW--	QHAKWFP--C--	
	351					400
cp-lap	Vvq1vKGrDY	VqkVlt....	
diap	Fu1laKGPAY	VseVlattaA	nasscpaTap	aptlq.....	
m-xiap	VlldeKQGQY	InnIhltbp.	LeEsLgrTas	kt.....Ppick	
xiap	VlldeKQGQY	InnIhltbp.	LeEsLgrTas	kt.....Ppick	
hiap1	VlldeKQGQY	InnIhltbp.	LeEsLgrTas	kt.....Ppick	
hiap2	VlldeKQGQY	InnIhltbp.	LeEsLgrTas	kt.....Ppick	
consensus	Vll---KQGQY	-----	L-E-L---T--	-----	-----P----	
	401					450
cp-lap	..acVLpge.	
diap	..adVLmdea	pakeAltLGl	dggvVrnald	rKl1ssGcaF	stldeLlhDi	
m-xiap	xIDdtifqnP	mVqeA1rMGF	sfxdlKkume	eKIqtsGssY	lslevLIaDL	
xiap	xIDdtifqnP	mVqeA1rMGF	sfxdlKkime	eKIqisGsnY	kslevLIaDL	
hiap1	seDaVMmntP	vInaAveMGF	srslVKqtvc	rKl1latGenY	rlvndIVlDI	
hiap2	seDaVMmntP	vVksAlaMGF	srslVKqtvc	rKl1latGenY	ktvndIVsaL	
consensus	--D-V----P	-V---A---MGF	----VK----	-KI---G---Y	-----LV-DL	
	451					500
cp-lap	
diap	fdcaqagaal	Evreppa...	
m-xiap	vsAqkDnteD	E.....	
xiap	vnAqkDsmcD	E.....	
hiap1	InAedE1reE	Ererateeke	snd1111rkn	rmalfqhlac	vlpildslit	
hiap2	InAedE1reE	Ekekqaeema	sdd1111rkn	rmalfqq1ac	vlpildn11k	
consensus	--A-----	E-----	-----	-----	-----	
	501					550
cp-lap	
diap	
m-xiap	
xiap	
hiap1	aq1neqend	v1kqktQtsL	Qare11d11	vkgn1aatvf	rns1qaaav	
hiap2	anv1nkqend	v1kqktQtsL	Qare11d11	vkgn1aaan1f	knd1k1endst	
consensus	-----	-----Q---L	Q-----	-----	-----	

	551		Ring Zinc Finger	600
cp-lap	...tki....Ekep	veDskLCKIC	yveEciVcFV
dlap	sniskitdei	ckmsvstpnq	nlslEenRq	LxDarLCKVC
m-xlapk	distEEQLRR	LqEEKLSKIC
xlapk	eistEEQLRR	LqEEKLCKIC
hlap1	lyehlfvccq	lkyiptedvs	dlpEEQLRR	LpEErtCKVC
hlap2	lyknlfwdkn	mkyiptedvs	glslEEQLRR	LqEErtCKVC
consensus	-----	-----	--S-EEQLRR	L-EE-LCK-C
	501			635
cp-lap	PCGHvVaCak	CAISVdKCPM	CRkIVtsvlk	vYFS.
dlap	PCGHLatCnq	CAPSVanCPM	CRadIkqfv	tFLS*
m-xlap	PCGHLatCkq	CAeaVdKCPM	CytVItfnqk	IFMS*
xlap	PCGHLVtCkq	CAeaVdKCPM	CytVItfkqk	IFMS*
hlap1	PCGHLVvCkd	CAPslrKCPi	CRstIkqtv	tFLS*
hlap2	PCGHLVvCqe	CAPslrKCPi	CRqIIkqtv	tFLS.
consensus	PCGHLV-C--	CA-SV-KCPM	CR--I-----	-FLS-

Fig. 8 (page 3 of 3)

Alignment of RZF (Ring Zinc Finger) Domains

Baculovirus	
Cp_iap	Cydia pomonella
Op_ap	Orgyia pseudotsugata
Human	
xiap	IAP on X chromosome
hiap1, hiap2	two different human IAP genes
Mouse	
m-xiap	mouse homologue of human xiap gene
Insect	
diap	Drosophila IAP gene, not clearly a homologue of xiap or hiap

FIG. 9

note on consensus:

The consensus line represents amino acids or very similar amino acids which are present in 6 of the 7 RZF sequences at each position. Capitalized residues are those that are in the consensus sequence.

SEQ ID NO:32	hiap2	1	EqlrrlqZer	tKVCMDkev	SVVFIPCGH1	VVCqeCApel	rkCPiC	46
SEQ ID NO:33	hiap1		EqltrlpZer	tKVCMDkev	SVVFIPCGH1	W CkdCAPs1	rkCPiC	
SEQ ID NO:34	m-xiap		EqltrlqZek	lSkICMDrnl	aiVFfPCGH1	atCkqCAeav	dkCPmC	
SEQ ID NO:35	xiap		EqltrlqZek	lCKICMDrnl	aiVFfPCGH1	vtCkqCAeav	dkCPmC	
SEQ ID NO:36	diap		EnrglkDar	lCKVCLdeev	gVVFIPCGH1	atCnqCApev	anCPmC	
SEQ ID NO:37	Cp_iap		EkepqqeDsk	lCKICyveec	iVCFvPCGHV	vaCakCALsv	dkCPmC	
SEQ ID NO:38	Op_iap		aveaevaDdr	lCKIClGack	tVCFvPCGHV	vaCgkCAagv	ttCPvC	
SEQ ID NO: 1	Consensus		E-----E--	-CKICM----	-V-F-PCGH-	--C--CA---	--CP-C	

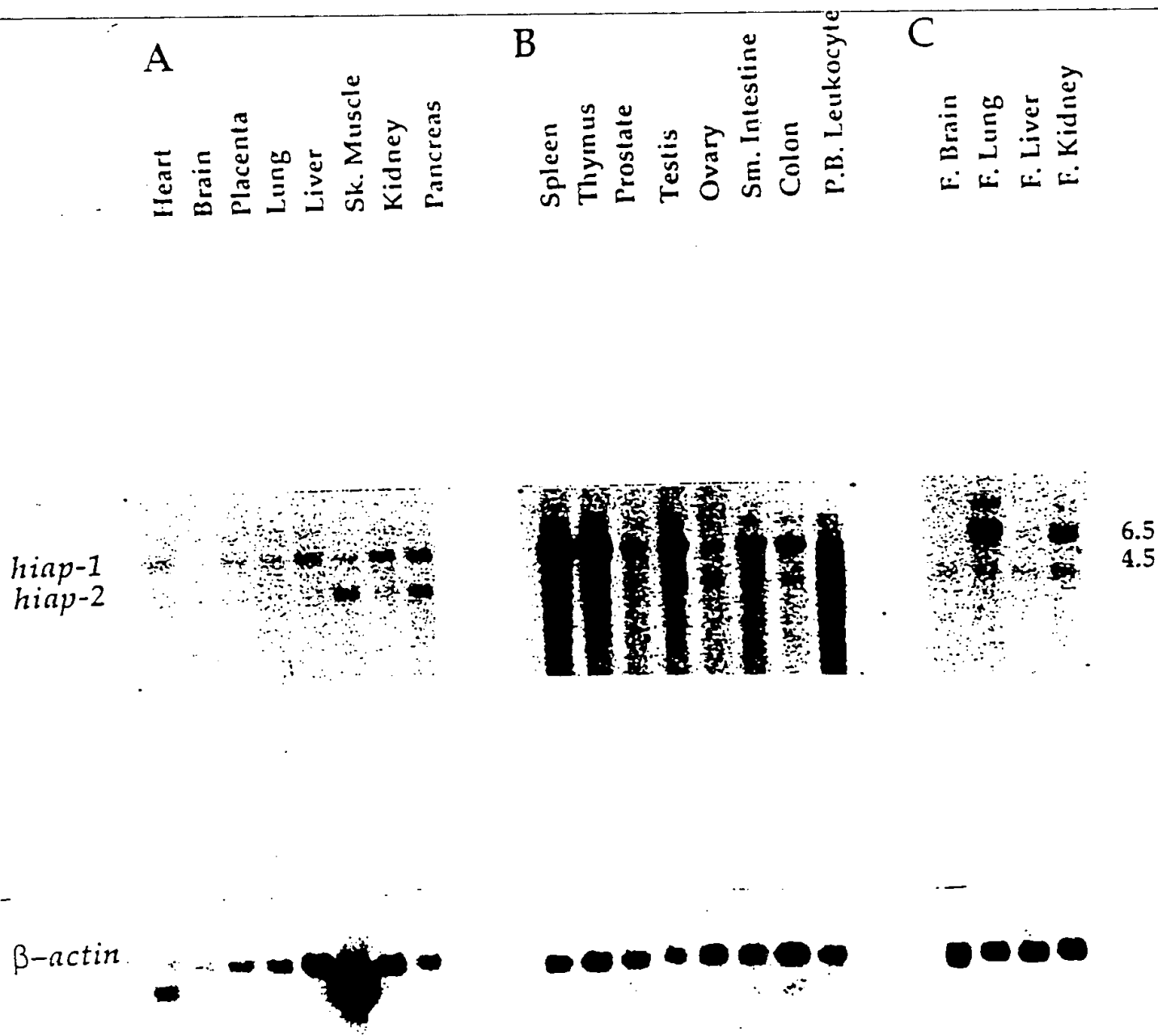


FIG. 10

007060" E4245960

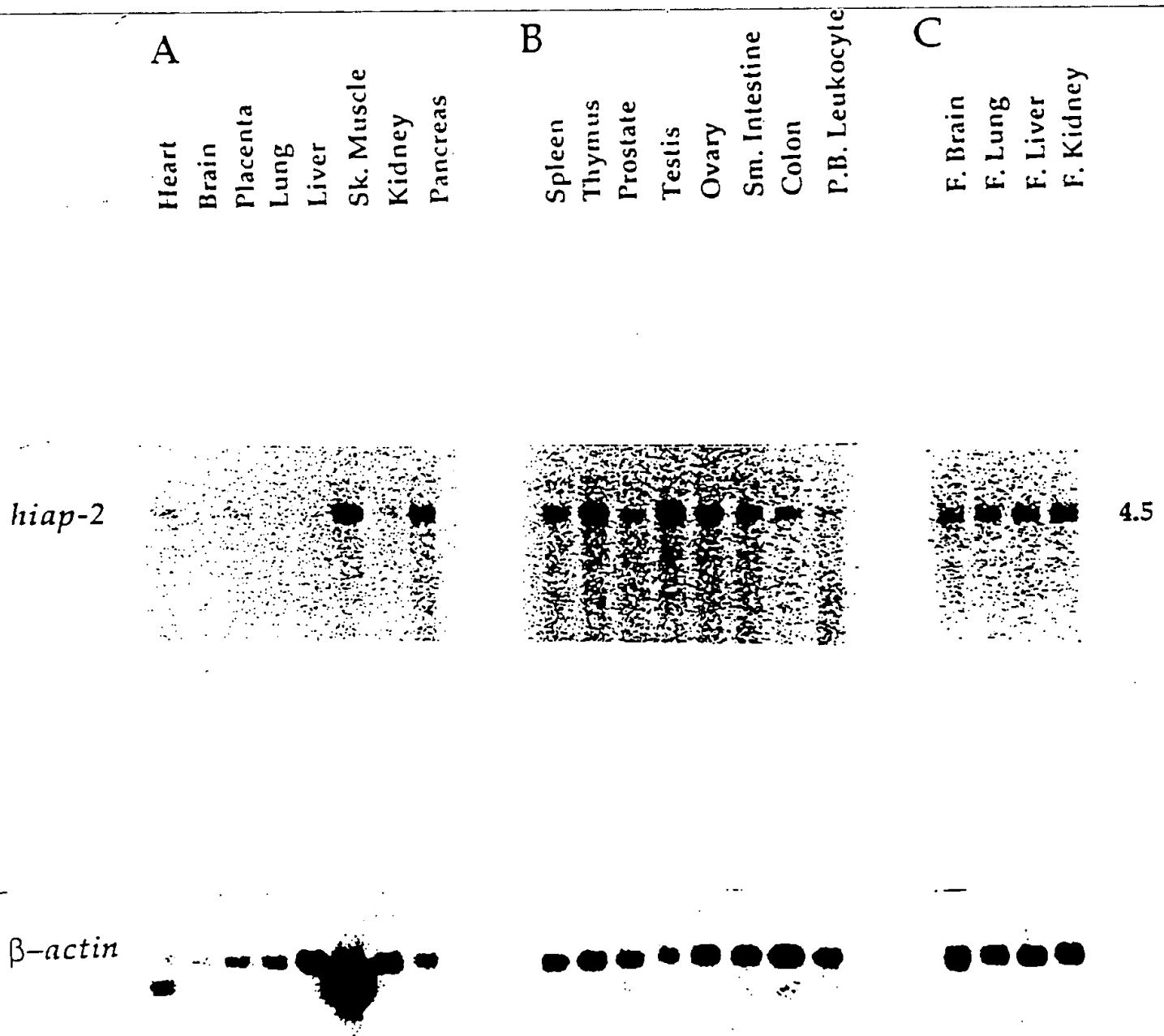


FIG. 11

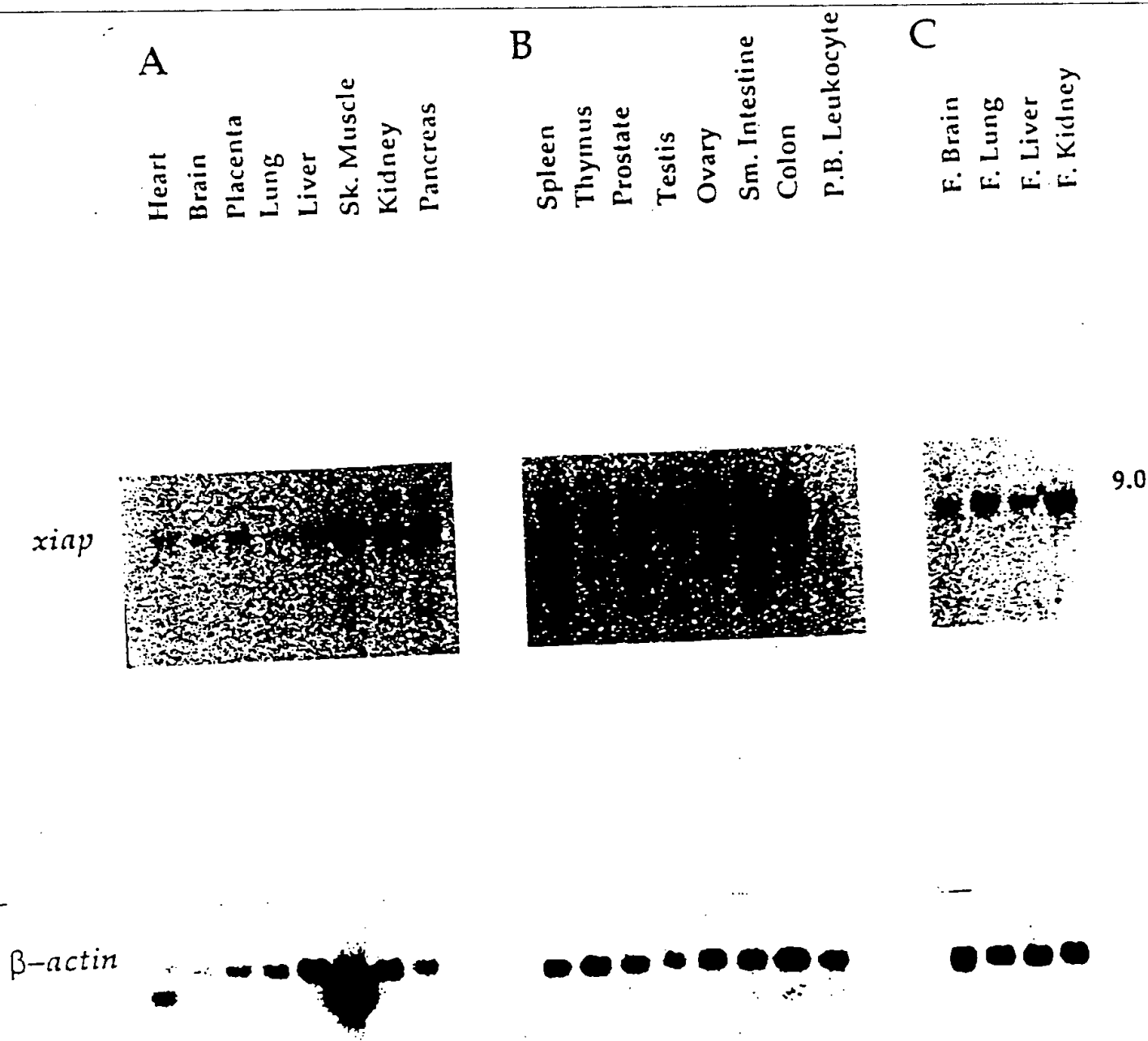
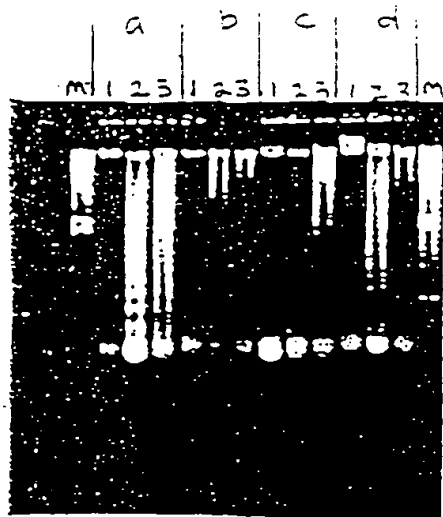


FIG. 12

00T060" E4245960

13A



13B

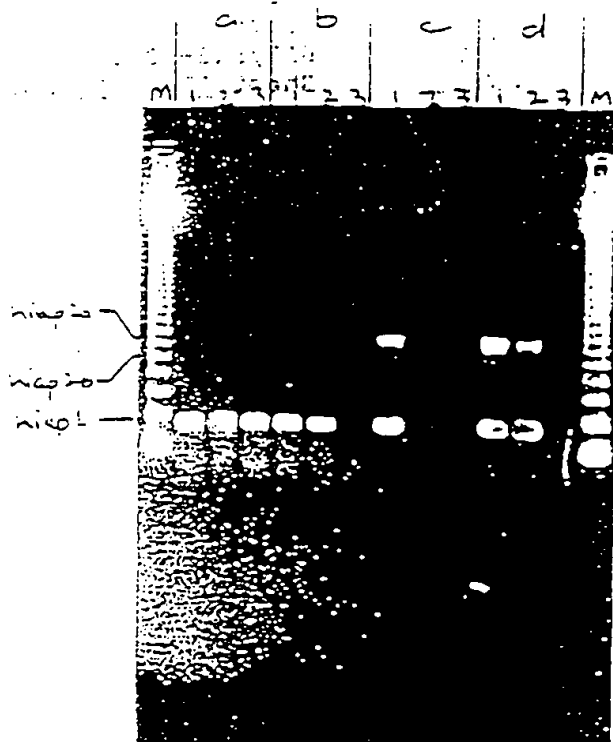
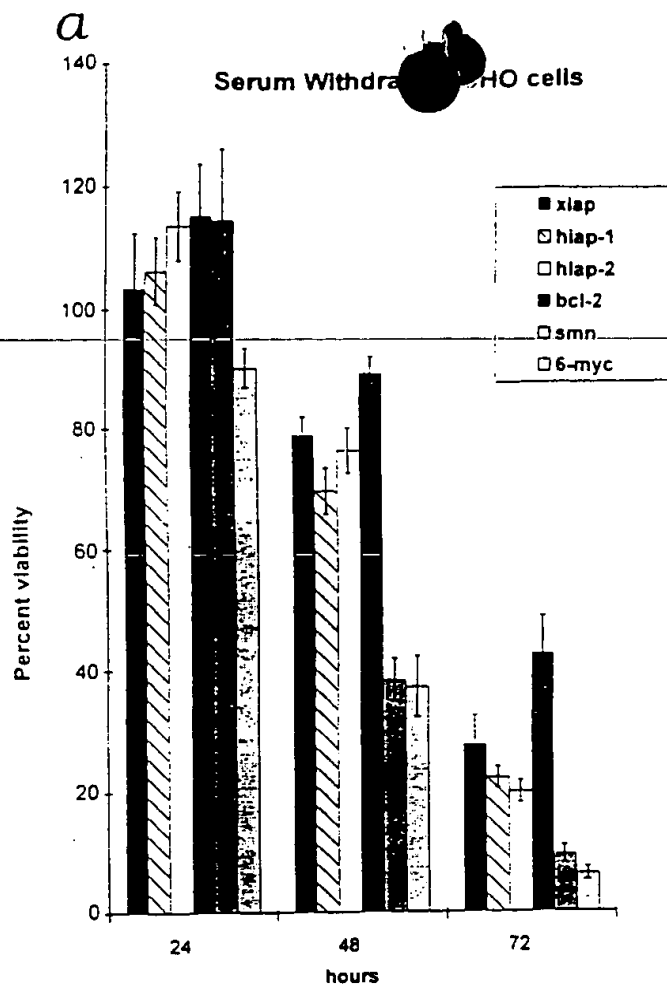
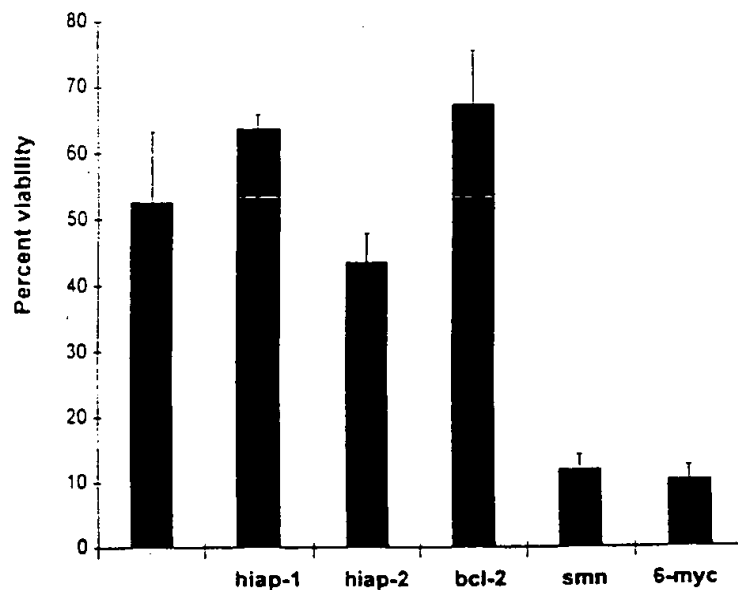


Fig. 13A and 13B



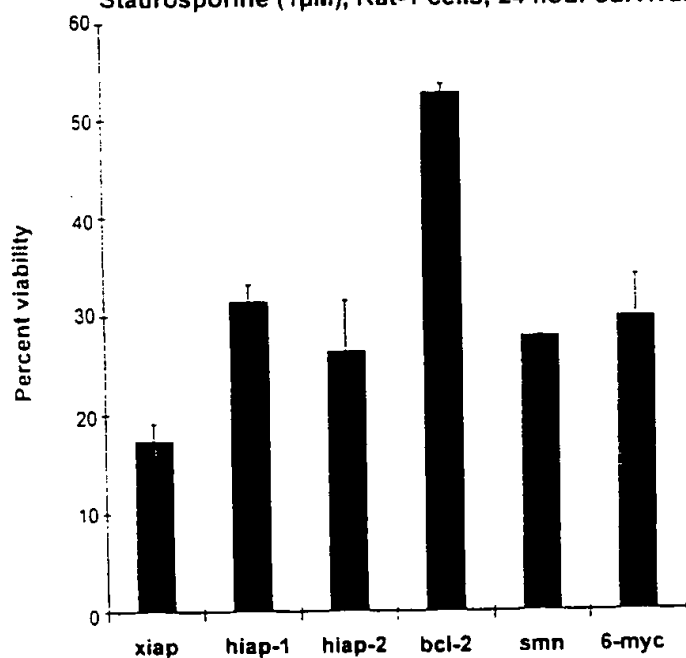
b

Menadione (20 μ M), CHO cells, 24 hr survival



c

Staurosporine (1 μ M), Rat-1 cells, 24 hour survival



d

Menadione (10 μ M), Rat-1 cells, 18 hour survival

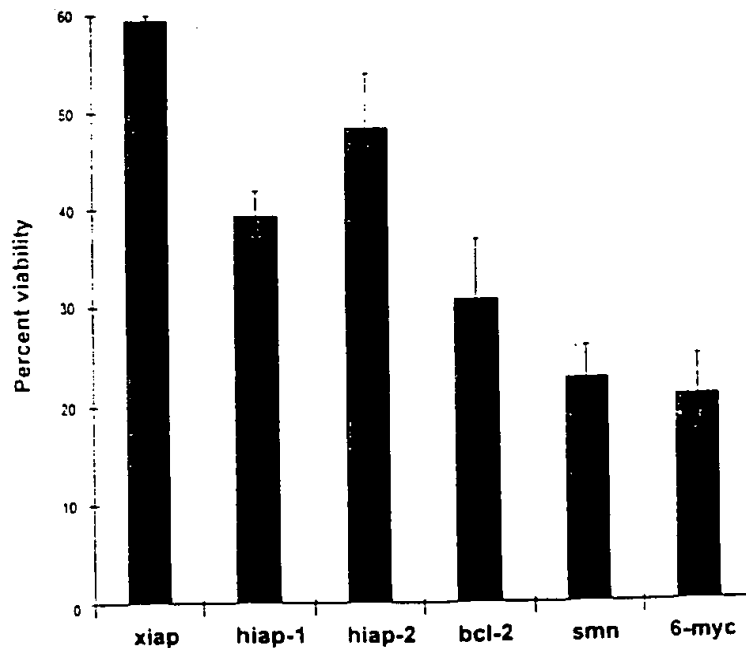


Fig. 14A - D